

What is claimed is:

1. A nucleic acid probe, comprising sequence of universal and designate nucleotides ordered in an iterative pattern.

2. The probe of claim 1, having a universal nucleotide selected from the group consisting of 5-nitroindole and 3-nitropyrrole.

3. The probe of claim 1, further comprising at least two contiguous designate nucleotides bound to an end of the sequence.

4. A set of nucleic acid probes, comprising a plurality of instances of a sequence of universal and designate nucleotides ordered in a pattern.

5. The set of nucleic acid probes of claim 4, wherein the pattern is iterative.

6. The set of nucleic acid probes of claim 4, comprising a universal nucleotide selected from the group consisting of 5-nitroindole and 3-nitropyrrole.

7a. The set of nucleic acid probes of claim 4, wherein the probes are displayed on a solid support.

7. A sequencing chip, comprising
a substrate, and
a set of nucleic acid probes disposed thereon, wherein each probe comprises an instance of a pattern of universal and designate nucleotides such that the set comprises a plurality of instances of the pattern.

8. The chip of claim 7, wherein the pattern is iterative.

9. The chip of claim 7, having a universal nucleotide selected from the group consisting of 5-nitroindole and 3-nitropyrrole.

10. The chip of claim 7, wherein each particular instance is associated with a particular location

on the chip.

11. The chip of claim 7, wherein each probe further comprises a sequence of at least two contiguous designate nucleotides bound to an end of the pattern.

12. Systems for ordering a set of hybridized probes, comprising
a probe detector capable of analyzing a substrate having a set of hybridized probes and capable of generating a spectrum signal representative of a set of subsequences associated with said set of hybridized probes, and

a sequencer for processing said spectrum signal, as a function of a predetermined pattern of designate and universal nucleotides associated with said set of hybridized probes, to organize said set of subsequences into sequential order.

13. A method for sequencing a nucleic acid sequence, comprising
providing a set of probes wherein each probe comprises an instance of a pattern of universal and designate nucleotides such that the set comprises a plurality of instances of the pattern,

determining a spectrum of probes representative of the probes in the set of probes which hybridize to a test sequence, and

ordering the spectrum of probes to determine a sequence of a portion of the test sequence.

14. A method for ordering a spectrum of probes to determine a sequence of a portion of a test sequence, comprising

i) providing a spectrum of probes that hybridize to a test sequence, wherein each probe in the spectrum is an instance of a pattern of universal and designate nucleotides, which pattern requires a designate nucleotide at an m^{th} position and an n^{th} position,

ii) identifying a first subset of probes from the spectrum whose first $m-1$ nucleotides correspond to a last $m-1$ nucleotides of a growing sequence,

iii) appending the nucleotide at the m^{th} position to the growing sequence if a single nucleotide occurs at the m^{th} position of all probes in the first subset.

15. The method of claim 14, further comprising

iv) if two or more nucleotides occur at the m^{th} position of the probes in the first subset,

designating a new growing sequence for each of the nucleotides which occur at the m^{th} position of the probes in the first subset, and

v) repeating the steps of identifying and appending for each new growing sequence until the step of identifying identifies zero probes.

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16. The method of claim 15, further comprising

iv) if two or more nucleotides occur at the m^{th} position of the probes in the first subset, selecting a second subset of probes from the spectrum whose first $n-1$ nucleotides correspond to a last $n-1$ nucleotides of the growing sequence, and

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v) appending a nucleotide to the growing sequence that uniquely occurs at the m^{th} position of the probes in the first subset and at the n^{th} position of the probes in the second subset.

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17. The method of claim 16, further comprising

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vi) if two or more nucleotides occur at the m^{th} position of the probes in the first subset and at the n^{th} position of the probes in the second subset, designating a new growing sequence for each of the nucleotides which occur at the m^{th} position of the probes in the first subset and at the n^{th} position of the probes in the second subset, and

vii) repeating steps ii) to v) for each new growing sequence until the step of identifying identifies zero probes.

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18. A computer-readable medium having stored thereon instructions for directing a computer to perform the acts of,

store a spectrum signal representative of a set of subsequences associated with said set of hybridized probes, wherein each subsequence represents an instance of a pattern of universal and designate nucleotides, which pattern designates a designate nucleotide at an m^{th} position and an n^{th} position,

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identify a first subset of said subsequences with beginning portions matching the last $m-1$ nucleotides of a growing sequence,

determine if each subsequence in said first set of subsequences includes the same type of

designate nucleotide in the m^{th} position, and

extending the growing sequence, as a function of the agreement of nucleotides in the m^{th} position, by a unit representative of ~~the~~ ^a nucleotide at the m^{th} position.

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